

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 14:44:37 ; Search time 814 Seconds

(without alignments)  
1863.490 Million cell updates/sec

Title: US-10-764-553-2

Perfect score: 1 cgcgcgcaccctgagatc.....gtgcgcaacgtgcgcgag 266

Sequence: 1 cgcgcgcaccctgagatc.....gtgcgcaacgtgcgcgag 266

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBankl :\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	266	100.0	80557	6 AX704276	AX704276 Sequence
C 2	266	100.0	110000	1 AE000516_28	Continuation (29 o
C 3	266	100.0	110000	1 AE000516_29	Continuation (30 o
C 4	266	100.0	307550	1 BX248343	Continuation (19 o
C 5	266	100.0	346051	1 BX842580	Continuation (18 o
C 6	134.4	50.5	303855	1 AE017230	Continuation (18 o
C 7	97.2	36.5	38807	1 MLCB1259	Continuation (18 o
C 8	97.2	36.5	40429	1 U00011	Continuation (18 o
C 9	97.2	36.5	40429	6 AR345357	Continuation (18 o
C 10	97.2	36.5	344050	1 MLEPRN2	Continuation (18 o
C 11	97.2	36.5	344050	1 AP006618_38	Continuation (18 o
C 12	97.2	36.5	344050	1 AP006618_39	Continuation (18 o
C 13	97.2	36.5	344050	1 BA000030_81	Continuation (18 o
C 14	65.4	24.6	110000	1 BA000030_81	Continuation (18 o
C 15	64.6	24.3	4312	1 SGA505987	Continuation (18 o
C 16	64	24.1	348408	1 BX248358	Continuation (18 o
C 17	61.2	23.0	3522	1 AF421216	Continuation (18 o
C 18	60.6	22.8	3350	1 SCAPTRBLA	Continuation (18 o

C 19	60.6	22.8	110000	1 CR931997_12	Continuation (13 o
C 20	60.6	22.8	277000	1 SC0939109	Continuation (13 o
C 21	59.8	22.5	110000	1 AE017282_08	Continuation (9 of
C 22	59.8	22.5	110000	1 CP000090_03	Continuation (4 of
C 23	58.8	22.1	555	6 BD164026	Continuation (18 o
C 24	58.8	22.1	555	6 AX121909	Continuation (18 o
C 25	58.8	22.1	555	6 AX064737	Continuation (18 o
C 26	58.8	22.1	13750	1 AF038651	Continuation (18 o
C 27	58.8	22.1	110000	1 BA000036_17	Continuation (18 o
C 28	58.8	22.1	349584	1 BX927153	Continuation (18 o
C 29	58.8	22.1	349584	6 AX127148	Continuation (18 o
C 30	57.4	21.6	4238	1 SCSECAPT	Continuation (18 o
C 31	57.2	21.5	190050	1 AL646059	Continuation (18 o
C 32	56.2	21.1	806	15 AK108481	Continuation (18 o
C 33	56.2	21.1	110000	1 BX571965_05	Continuation (18 o
C 34	56.2	21.1	110000	1 CP000010_31	Continuation (18 o
C 35	55.4	20.8	110000	1 AP008231_17	Continuation (18 o
C 36	55	20.7	346259	1 BX640435	Continuation (18 o
C 37	55	20.7	346287	1 BX640450	Continuation (18 o
C 38	54.6	20.5	297050	1 AL935258	Continuation (18 o
C 39	54.2	20.4	79370	3 UNK431260	Continuation (18 o
C 40	53.6	20.2	303642	1 AE016923	Continuation (18 o
C 41	53.4	20.1	346359	1 BX640411	Continuation (18 o
C 42	52.4	19.7	110000	1 CP000009_08	Continuation (9 of
C 43	52.4	19.7	110000	1 CP000009_09	Continuation (10 o
C 44	52.2	19.6	489	6 AX432181	Continuation (28 o
C 45	52.2	19.6	110000	1 AE017333_27	Continuation (28 o

## ALIGNMENTS

RESULT 1	AX704276	80557 bp	DNA	linear	PAT 03-APR-2003
LOCUS	AX704276	Sequence 647 from Patent WO02074903.			
DEFINITION	AX704276				
ACCESSION	AX704276.1	GI:29538531			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
INSTITUT PASTEUR (FR)					
Patent: WO 02074903-A 647 26-SEP-2002;					
Location/Qualifiers					
1. 80557					
/organism="Mycobacterium tuberculosis"					
/mol_type="unassigned DNA"					
/db_xref="taxon:1773"					
/note="BAC-RV234 deposited at the C.N.C.M. under the A.N. I-2627"					

## ORIGIN

Query Match	100.0%	Score 266;	DB 6;	Length 80557;
Best Local Similarity	100.0%	Pred. No. 7.7e-31;		
Matches	266;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
1	CGCGGCACTTCGAGATTCTCGCTGAGGGCATCGAGTTGCGGGCCCGCTGTGAT	60		
62589	CGCGGCACTTCGAGATTCTCGCTGAGGGCATCGAGTTGCGGGCCCGCTGTGAT	62530		
61	CATTGACGAGTGTAGCAACCGGCGGACGATCGGCGGACGCGGCTGCTGAGG	120		
62529	CATTGACGAGTGTAGCAACCGGCGGACGATCGGCGGACGCGGCTGCTGAGG	62470		
121	CGGTGCGGCAACGTTGCGGCGGCGGCGGCTGAGTGTGAACTTGCGGGTTGAGCGGTG	180		

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 14:18:52, Search time 367 Seconds

(without alignment)  
4830.540 Million cell updates/sec

Title: US-10-764-553-2

Perfect score: 266  
Sequence: 1 cgcgcgcacctcgcgagatc.....ggtcgcgaacgtgcgcgag 266

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4896997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N\_Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES.

Result No.	Score	Query Match	Length	ID	Description
1	266	100.0	266	14 ADZ65097	Adz65097 Mycobacte
2	266	100.0	1874	14 ADZ65096	Adz65096 Mycobacte
3	266	100.0	80557	4 ABX09142	ABX09142 Mycobacte
4	266	100.0	110000	6 AA199682_29	Continuation (30 o
5	266	100.0	110000	4 AA199683_28	Continuation (30 o
6	266	100.0	110000	4 AA199683_29	Continuation (30 o
7	266	100.0	110000	4 AA199683_29	Continuation (30 o
8	266	100.0	110000	4 AA199683_29	Continuation (30 o
9	266	100.0	110000	4 AA199683_29	Continuation (30 o
10	266	100.0	110000	4 AA199683_29	Continuation (30 o
11	266	100.0	110000	4 AA199683_29	Continuation (30 o
12	266	100.0	110000	4 AA199683_29	Continuation (30 o
13	266	100.0	110000	4 AA199683_29	Continuation (30 o
14	266	100.0	110000	4 AA199683_29	Continuation (30 o
15	266	100.0	110000	4 AA199683_29	Continuation (30 o
16	266	100.0	110000	4 AA199683_29	Continuation (30 o
17	266	100.0	110000	4 AA199683_29	Continuation (30 o
18	266	100.0	110000	4 AA199683_29	Continuation (30 o
19	266	100.0	110000	4 AA199683_29	Continuation (30 o

20	48.6	18.3	660	11	ACH99807	ACH99807 Klebsiell
21	48.4	18.2	450	13	AD63368	AD63368 Bacterial
22	48.4	18.2	456	13	AD63375	AD63375 Bacterial
23	47.2	17.7	546	13	AD559951	AD559951 Bacterial
24	47.2	17.7	546	13	AD555671	AD555671 Bacterial
25	47.2	17.7	546	13	AD550157	AD550157 Bacterial
26	47.2	17.7	546	13	AD556186	AD556186 Bacterial
27	46.6	17.5	516	9	AD810513	AD810513 Altiococ
28	46.6	17.5	516	9	AD810513	AD810513 Altiococ
29	46.2	17.4	570	13	AD61694	AD61694 Bacterial
30	46.2	17.3	546	13	AD61867	AD61867 Bacterial
31	45.6	17.1	18538	14	AC164706	AC164706 M. Xanthu
32	45.2	17.0	552	10	AD676492	AD676492 APRT reco
33	45.2	17.0	552	10	AD676490	AD676490 APRT reco
34	45.2	17.0	552	13	AD645994	AD645994 Bacterial
35	45.2	17.0	1617	5	AA590127	AA590127 DNA encod
36	45.2	16.9	615	13	AD745732	AD745732 Bacterial
37	45.2	16.9	1511	13	AD717106	AD717106 Plant CDN
38	44.8	16.8	516	6	ABN67362	ABN67362 Streptoco
39	44.8	16.8	110000	6	ABN71527	ABN71527 Streptoco
40	44.6	16.8	516	13	AD742451	AD742451 Pseudomon
41	44.4	16.7	426	11	ABD07932	ABD07932 Pseudomon
42	44.4	16.7	504	13	AD747054	AD747054 Bacterial
43	44.4	16.7	549	10	AD762246	AD762246 P.aerugin
44	44.4	16.7	549	10	AD762248	AD762248 P.aerugin
45	44.4	16.7	549	14	AE10906	AE10906 Pseudomon

## ALIGNMENTS

RESULT 1  
ID ADZ65097 standard; DNA; 266 BP.

ADZ65097;

14-JUL-2005 (first entry)

Mycobacterium tuberculosis real/spot upstream DNA fragment.

promoter; high throughput screening; antibacterial; ds.

Mycobacterium tuberculosis.

US2005095252-A1.

05-MAY-2005.

27-JAN-2004; 2004US-00764553.

27-JAN-2003; 2003US-044251P.

(COUN-) COUNCIL SCI & IND RES INDIA.

Chatterjee D;

WPI; 2005-344982/35.

New promoter derived from Mycobacterium tuberculosis, useful for high throughput screening and developing inhibitors of M. tuberculosis under low carbon or starved conditions.

Claim 1; SEQ ID NO 2; 20pp; English.

The invention relates to a promoter (I) for high throughput screening and developing inhibitors of Mycobacterium tuberculosis under low carbon or starved conditions, and having the 266 base pair sequence of ADZ65097. Also described: (1) an expression system (II) for high-throughput screening and developing inhibitors of Mycobacterium tuberculosis under low carbon or starved conditions, comprising of promoter of 200 base pair having ADZ65097 in a vector pSAL12; and (2) preparing a promoter expression system for high-throughput screening and developing inhibitors against Mycobacterium tuberculosis.

Query Match	22.5%	Score 59.8	DB 1	Length 565
Best Local Similarity	59.9%	Pred. No. 0.0029		
Matches 100; Conservative	0;	Mismatches 67;	Indels 0;	Gaps 0

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 15:45:49 ; Search time 89 Seconds  
(without alignments)  
5312.712 Million cell updates/sec

Title: US-10-764-553-2

Perfect score: 266  
Sequence: 1 CGCGCCGCTCGGAGATTC.....GGTGCAGCACTGCGCGAG 266

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/P COMB.seq:\*
- 7: /cgn2\_6/prodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/prodata/1/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	266	100.0	4403765	3	US-09-103-840A-2
C 2	266	100.0	4411529	3	US-09-103-840A-1
C 3	97.2	36.5	40429	3	US-08-311-731A-125
C 4	48.6	18.3	660	3	US-09-489-039A-55602
C 5	45.6	17.1	18538	3	US-09-902-540-1169
C 6	44.4	16.7	426	3	US-09-252-991A-6536
C 7	44.4	16.7	714	3	US-09-252-991A-6536
C 8	42.6	16.0	2598	3	US-09-902-540-3087
C 9	42.6	16.0	6888	3	US-09-902-540-862
C 10	42.4	15.9	1794	3	US-09-902-540-9281
C 11	42.4	15.9	10717	3	US-09-902-540-991
C 12	40.8	15.3	405	3	US-09-252-991A-7491
C 13	40.8	15.3	522	3	US-09-252-991A-7206
C 14	40.8	15.3	669	3	US-09-252-991A-7270
C 15	40.8	15.3	780	3	US-09-252-991A-7431
C 16	40.4	15.2	4403765	3	US-09-103-840A-2
C 17	40.4	15.2	4411529	3	US-09-103-840A-1
C 18	40	15.0	837	3	US-09-902-540-2787
C 19	40	15.0	15644	3	US-09-902-540-1123
C 20	39.8	15.0	855	3	US-09-252-991A-11835
C 21	39.8	15.0	1497	3	US-09-252-991A-11611
C 22	39.8	15.0	4756	3	US-09-023-655-1461
C 23	39.8	15.0	5117	3	US-08-854-585-1
C 24	39.8	15.0	5117	3	US-09-447-533-1

C 25	39.8	15.0	5117	6	PCT-US95-05512-1	Sequence 1, Appli
C 26	39.8	15.0	7560	3	US-09-754-112A-2	Sequence 2, Appli
C 27	39.8	15.0	12738	3	US-09-754-112A-1	Sequence 1, Appli
C 28	39.6	14.9	903	3	US-09-902-540-9555	Sequence 9555, Ap
C 29	39.6	14.9	9867	3	US-09-902-540-1008	Sequence 1008, Ap
C 30	39.4	14.8	339	3	US-09-621-976-44	Sequence 44, Appli
C 31	39.4	14.8	1754	3	US-10-000-489-83	Sequence 83, Appli
C 32	39.4	14.8	1754	3	US-10-000-489-83	Sequence 85, Appli
C 33	39.4	14.8	1855	3	US-10-000-489-85	Sequence 97, Appli
C 34	38.8	14.6	73853	3	US-09-949-016-12029	Sequence 12029, A
C 35	38.6	14.5	534	3	US-09-107-532A-2574	Sequence 2574, Ap
C 36	38.6	14.5	1710	2	US-08-912-794-1	Sequence 1, Appli
C 37	38.6	14.5	129658	3	US-09-949-016-11195	Sequence 17195, A
C 38	38.4	14.4	530	3	US-08-758-662-4	Sequence 4, Appli
C 39	38.4	14.4	4524	2	US-08-845-998-7	Sequence 7, Appli
C 40	38.4	14.4	4524	3	US-09-206-537-7	Sequence 7, Appli
C 41	38.4	14.4	4524	3	US-09-430-854-7	Sequence 7, Appli
C 42	38.2	14.4	927	3	US-09-252-991A-7558	Sequence 7558, Ap
C 43	38.2	14.4	1155	3	US-09-252-991A-7856	Sequence 7856, Ap
C 44	38	14.3	1491	3	US-09-902-540-3335	Sequence 3335, Ap
C 45	38	14.3	16387	3	US-09-902-540-1156	Sequence 1156, Ap

## ALIGNMENTS

RESULT 1									
US-09-103-840A-2/c									
Sequence 2, Application US/09103840A									
Patent No. 6234328									
GENERAL INFORMATION:									
APPLICANT: FLEISCHMAN, Robert D.									
APPLICANT: WHITE, Owen R.									
APPLICANT: FRASER, Claire M.									
APPLICANT: VENTER, John C.									
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM									
FILE REFERENCE: 24366-20007.00									
CURRENT APPLICATION NUMBER: US/09/103,840A									
NUMBER OF SEQ ID NOS: 2									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 2									
LENGTH: 4403765									
TYPE: DNA									
ORGANISM: Mycobacterium tuberculosis									
FEATURE:									
OTHER INFORMATION: CDC 1551									
OTHER INFORMATION: "n" bases at various positions throughout the sequence									
OTHER INFORMATION: represent a, t, c or g									
US-09-103-840A-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 8e-53; Length 4403765;									
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CGCGCCGCTCGGAGATTCGCTGAGAGGCGATCGAGCTTCGGGCGCGCTGCTGAT	60						
DB	2906559	CGCGCCGCTCGGAGATTCGCTGAGAGGCGATCGAGCTTCGGGCGCGCTGCTGAT	2906500						
QY	61	CATTGACGACGTTGAGCAACCGCGGACCATCGGCGGACGCGACGCGCTGTTGACG	120						
DB	2906499	CATTGACGACGTTGAGCAACCGCGGACCATCGGCGGACGCGACGCGCTGTTGACG	2906440						
QY	121	CGGTGCGCCGCAACGTTGAGCAACCGCGGACCATCGGCGGACGCGCTGTTGACG	180						
DB	2906439	CGGTGCGCCGCAACGTTGAGCAACCGCGGACCATCGGCGGACGCGCTGTTGACG	2906380						
QY	181	CGCGGCGCTCGGAGATTCGCTGAGAGGCGATCGAGCTTCGGGCGCGCTGCTGAT	240						
DB	2906379	CGCGGCGCTCGGAGATTCGCTGAGAGGCGATCGAGCTTCGGGCGCGCTGCTGAT	2906320						
QY	241	GTCGAGGTGACGAACGTTGAGCAACCGCGGACCATCGGCGGACGCGCTGTTGACG	266						



ORGANISM: *Corynebacterium glutamicum*

241 GTCGAGGTGACGAACGTGCCGAGG 266



DB 2906319 GTCCGAGGTGACGACGCTGGCCGAGG 2906294

## RESULT 2

US-09-103-840A-1/c  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 2436-2007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 100.0%; Score 266; DB 3; Length 4411529;  
Best Local Similarity 100.0%; Pred. No. 8e-53;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCGCACTCTGAGATTCTCGCTGAGGCGATCGAGGTCGGGCGCCGCTGTCTGAT 60  
DB 2910452 CGCCGCACTCTGAGATTCTCGCTGAGGCGATCGAGGTCGGGCGCCGCTGTCTGAT 2910393  
QY 61 CATTGAGAGTGTACCAACCGGCGGACCATGCGGCGACCGGACGCGCTGCTTGAACG 120  
DB 2910392 CATTGAGAGTGTACCAACCGGCGGACCATGCGGCGACCGGACGCGCTGCTTGAACG 2910333  
QY 121 CGGTGGCGCCAGCTGGCGCGGCGCGCTGTGTGAACTTTCGGGGGTTGACGGTTCG 180  
DB 2910332 CGGTGGCGCCAGCTGGCGCGGCGCGCTGTGTGAACTTTCGGGGGTTGACGGTTCG 2910273  
QY 181 CGCGGCGCTGCGACCGCTGCGGCGGACGCTGAGCGCGCTGTGAGGATATCTCTAG 240  
DB 2910272 CGCGGCGCTGCGACCGCTGCGGCGGACGCTGAGCGCGCTGTGAGGATATCTCTAG 2910213  
QY 241 GTCCGAGGTGACGACGCTGGCCGAGG 266  
DB 2910212 GTCCGAGGTGACGACGCTGGCCGAGG 2910187

## RESULT 3

US-08-311-731A-125/c  
Sequence 125, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:  
LENGTH: 40429 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-125

Query Match 36.5%; Score 97.2; DB 3; Length 40429;  
Best Local Similarity 68.3%; Pred. No. 1e-13;  
Matches 149; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

QY 4 CGCCACTCTGAGATTCTCGCTGAGGCGATCGAGGTTGCGGCGCCGCTGTCTGATCAT 63  
DB 9392 CGGCATATGAGAGTACCCGCTGACAGCGTCAAGACCGCAACGTGTGATTAAT 9333  
QY 64 TACAGAGTGTGACCAACCGGCGGACCATGCGGCGACGCGCTGCTTGAACGCGG 123  
DB 9332 TACAGAGTGTGACCAACCGGCGGACCATGCGGCGTGTGTGCGGATTAATGAGGCGAG 9273  
QY 124 TGGCGCAACGTGCGCGGCGGCGCGCTA-GTGTGAACTTTCGGGGTTCAGCGGTGCG 182  
DB 9272 CGGTTCGGGTCCATTGCGGCGGCGGCTGTGTGAACTTTCAGGCGGTGCGGCG 9213  
QY 183 CGGCGCTGCGACCGCTGCGGCGGACGCTGAGCGCGC 220  
DB 9212 AGCGCATGCGACCGCTGCGAGGTACAAAGTTGAGCGCG 9175

## RESULT 4

US-09-489-039A-5602  
Sequence 5602, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 5602  
LENGTH: 660  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5602

Query Match 18.3%; Score 48.6; DB 3; Length 660;  
Best Local Similarity 54.3%; Pred. No. 0.015; 99; Indels 3; Gaps 1;  
Matches 121; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

QY 1 CGCCGCACTCTGAGATTCTCGCTGAGGCGATCGAGGTTGCGGCGCCGCTGTCTGAT 60